

Fig 1A. ScFv library

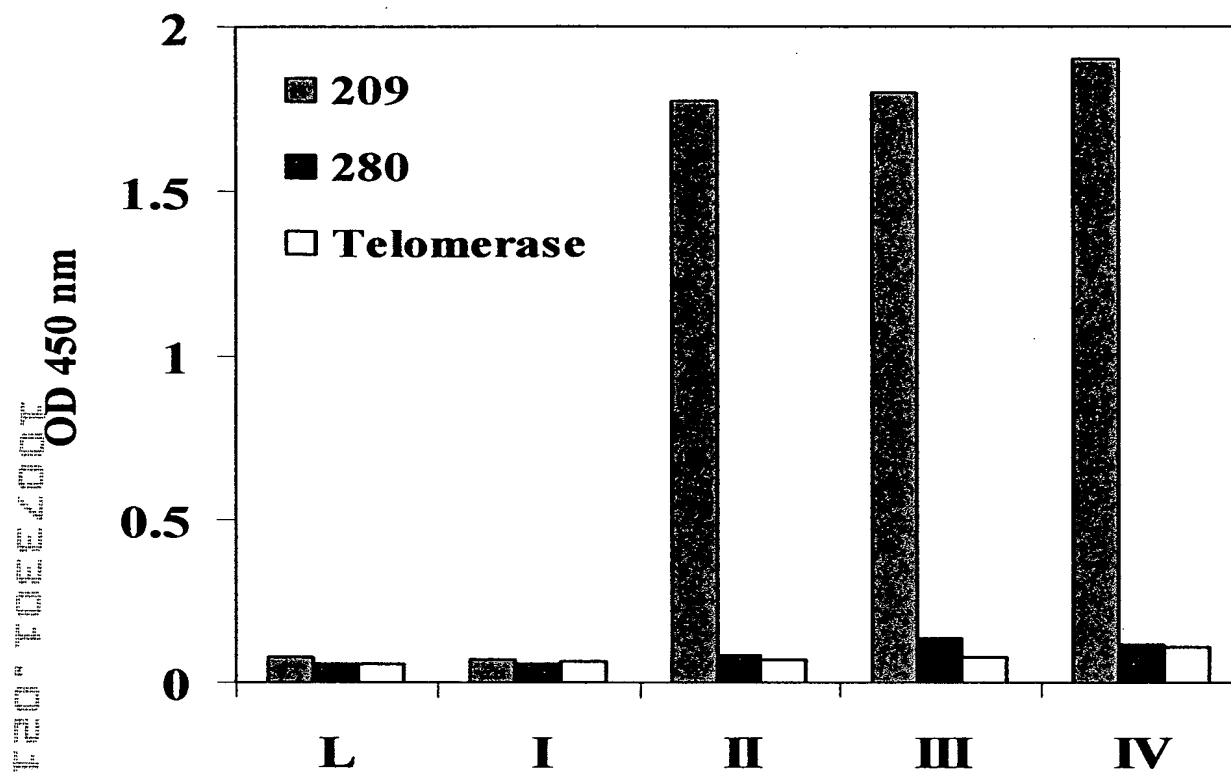


Fig 1B. ScFv-CBD library

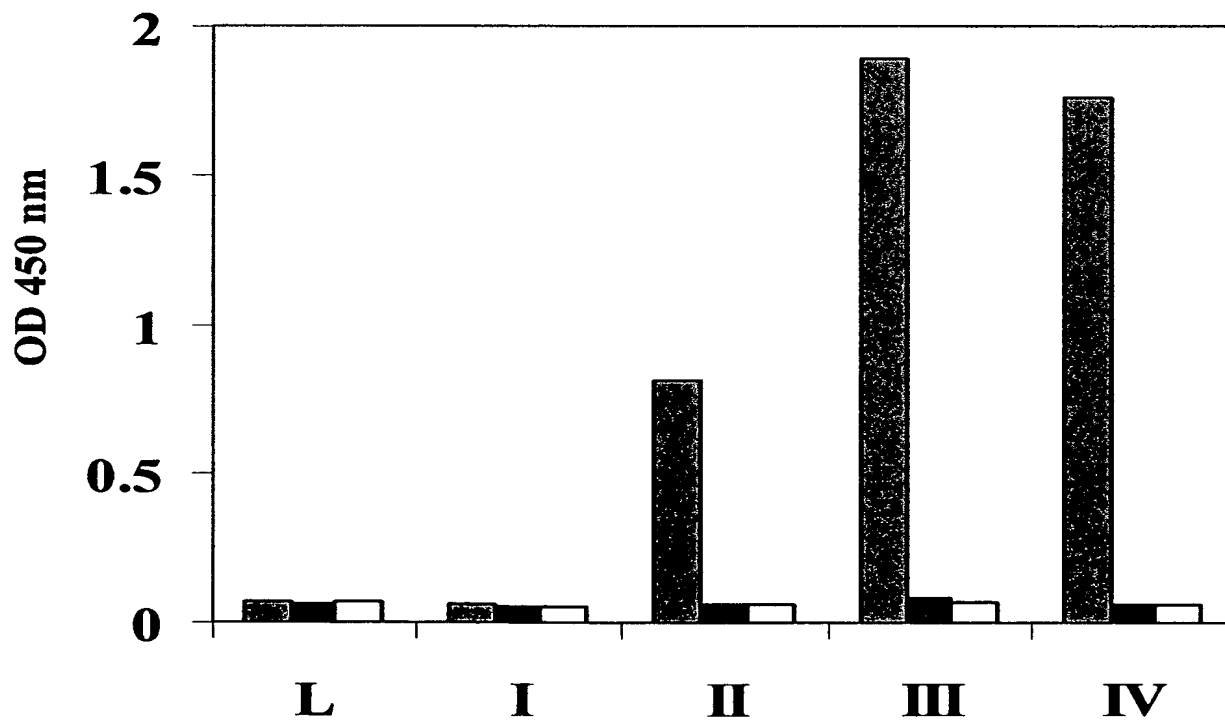


Fig. 2A. HLA-A2/G9-209

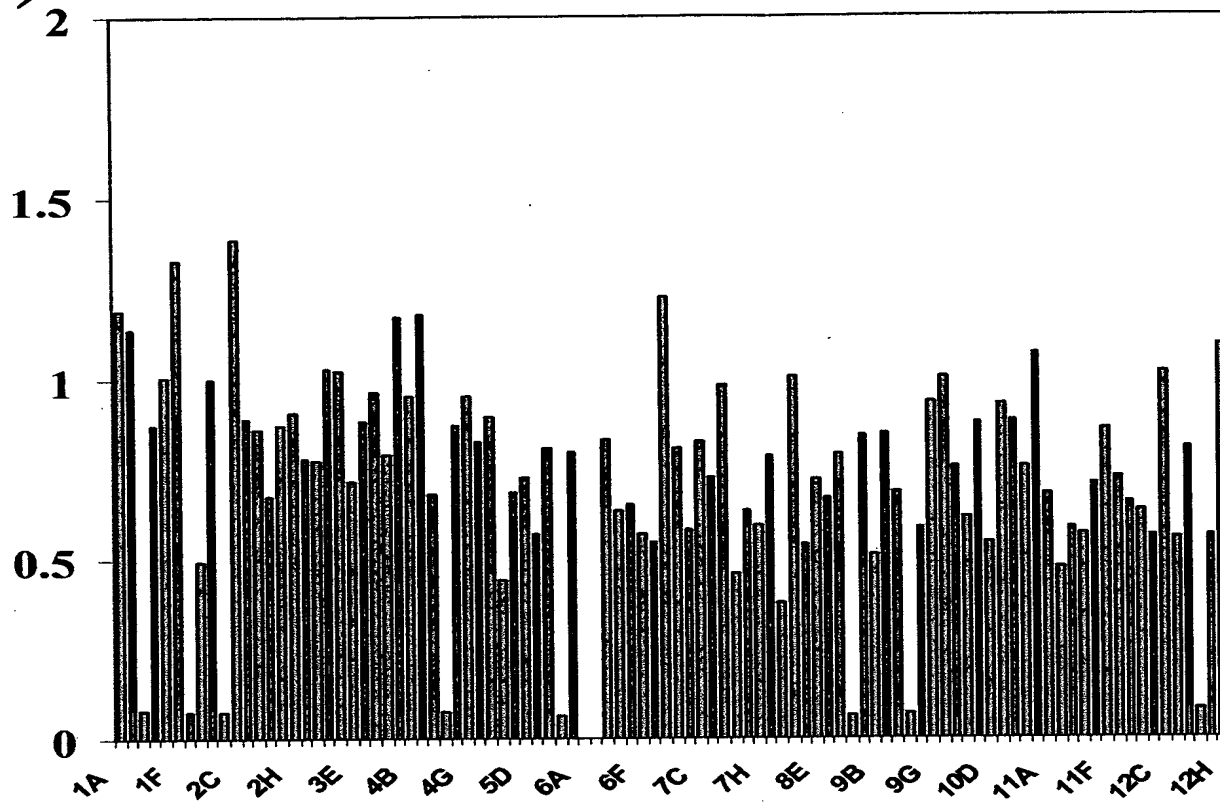
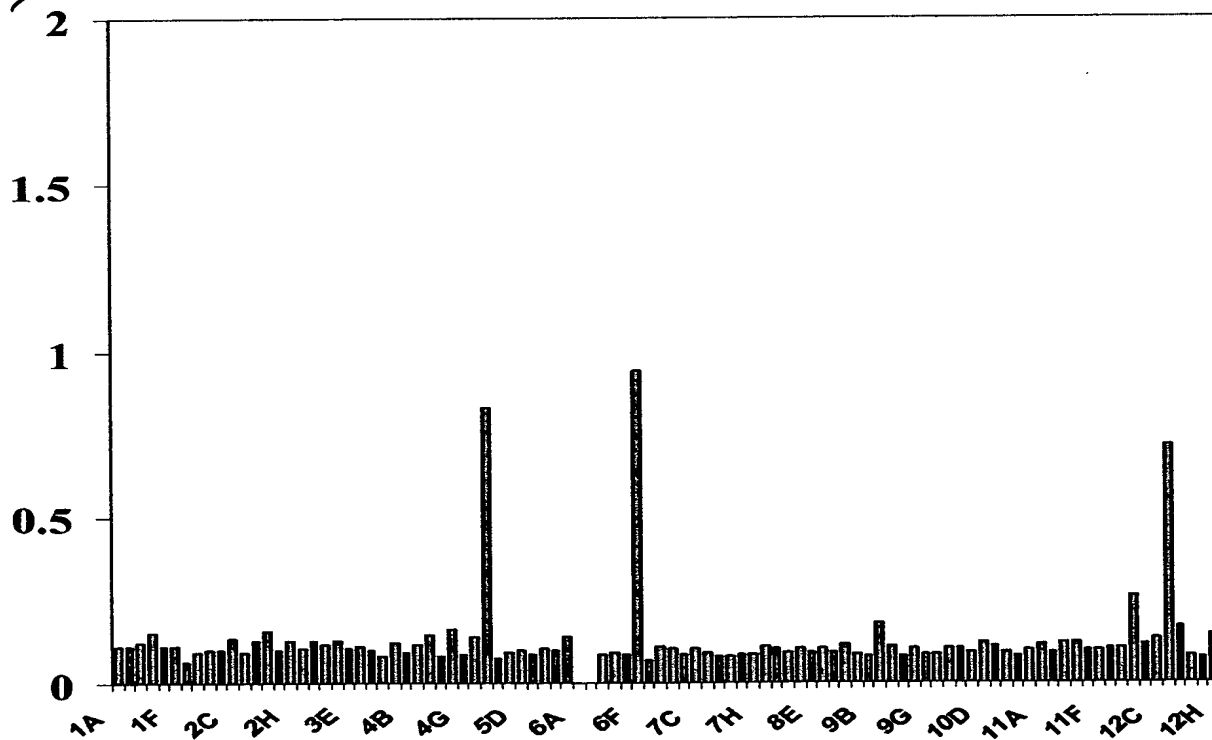


Fig. 2B. HLA-A2/G9-280



[illegible]

1	2	3	4	5	6	7	8	9	10	11	12	13	14	SEQ ID NO:8	SEQ ID NO:9
CAG	GTG	AAA	CTG	CAG	GAG	TCT	GGG	GGA	GGC	TTA	GTG	AAG	CCT	SEQ ID NO:8	SEQ ID NO:9
gln	val	lys	leu	gln	glu	ser	gly	gly	gly	leu	val	lys	pro		
15	16	17	18	19	20	21	22	23	24	25	26	27	28		
GGA	GGG	TCC	CTG	AAA	CTC	TCC	TGT	GCA	GCC	TCT	GGA	TTC	ACT		
gly	gly	ser	leu	lys	leu	ser	cys	ala	ala	ser	gly	phe	thr		
29	30	31	32	33	34	35	36	37	38	39	40	41	42		
TTC	AGT	AGC	TAT	GGC	ATG	TCT	TGG	GTT	CGC	CAG	ACT	CCA	GAC		
phe	ser	ser	tyr	gly	met	ser	trp	val	arg	gln	thr	pro	asp		
43	44	45	46	47	48	49	50	51	52	53	54	55	56		
AAG	AGG	CTG	GAG	TGG	GTC	GCA	ACC	ATT	AGT	AGT	GGT	GGT	AGT		
lys	arg	leu	glu	trp	val	ala	thr	ile	ser	ser	gly	gly	ser		
57	58	59	60	61	62	63	64	65	66	67	68	69	70		
TAC	ACC	TAC	TAT	CCA	GAC	AGT	GTG	AAG	GGG	CGA	TTC	ACC	ATC		
tyr	thr	tyr	tyr	pro	asp	ser	val	lys	gly	arg	phe	thr	ile		
71	72	73	74	75	76	77	78	79	80	81	82	83	84		
TCC	AGA	GAC	AAT	GCC	AAG	AAC	ACC	CTG	TAC	CTG	CAA	ATG	AGC		
ser	arg	asp	asn	ala	lys	asn	thr	leu	tyr	leu	gln	met	ser		
85	86	87	88	89	90	91	92	93	94	95	96	97	98		
AGT	CTG	AAG	TCT	GAG	GAC	ACA	GCC	ATG	TAT	TAC	TGT	GCA	AGA		
ser	leu	lys	ser	glu	asp	thr	ala	met	tyr	tyr	cys	ala	arg		
99	100	101	102	103	104	105	106	107	108	109	110	111	112		
GGT	AAC	TGG	GAA	GGA	TGG	TAC	TTC	GAT	GTC	TGG	GGC	CAA	GGG		
gly	asn	trp	glu	gly	trp	tyr	phe	asp	val	trp	gly	gln	gly		
113	114	115	116	117	118										
ACC	ACG	GTC	ACC	GTC	TCC	TCA	GGT	GGA	GGC	GGT	TCA	GGC	GGA		
thr	thr	val	thr	val	ser	<u>ser</u>	<u>gly</u>	<u>gly</u>	<u>gly</u>	<u>gly</u>	<u>ser</u>	<u>gly</u>	<u>gly</u>		
									1	2	3	4	5	6	
GGT	GGC	TCT	GGC	GGT	GGC	GGA	TCG	AAC	ATC	GAG	CTC	ACT	CAG		
<u>gly</u>	<u>gly</u>	<u>ser</u>	<u>gly</u>	<u>gly</u>	<u>gly</u>	<u>gly</u>	<u>ser</u>	asn	ile	glu	leu	thr	gln		
7	8	9	10	11	12	13	14	15	16	17	18	19	20		
TCT	CCA	GCA	ATC	ATG	TCT	GCA	TCT	CCA	GGG	GAG	AGG	GTC	ACC		
ser	pro	ala	ile	met	ser	ala	ser	pro	gly	glu	arg	val	thr		
21	22	23	24	25	26	27	28	29	30	31	32	33	34		
ATG	ACC	TGC	AGT	GCC	AGC	TCA	AGT	ATA	CGT	TAC	ATA	TAT	TGG		
met	thr	cys	ser	ala	ser	ser	ser	ile	arg	tyr	ile	tyr	trp		
35	36	37	38	39	40	41	42	43	44	45	46	47	48		

FIGURE 3A(ii)

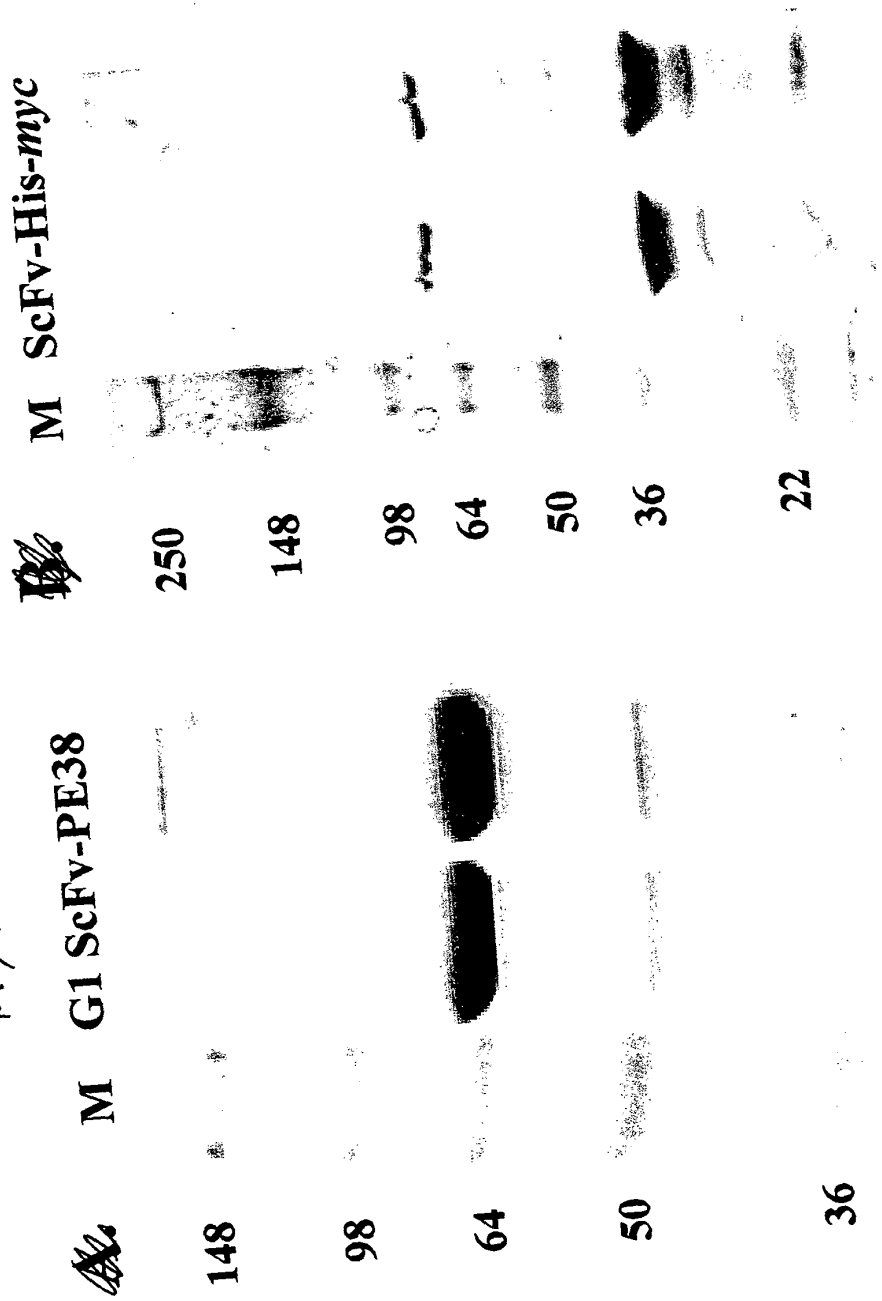
63	64	65	66	67	68	69	70	71	72	73	74	75	76
GGC	AGT	GGG	TCT	GGG	ACC	TCT	TAT	TCT	CTC	ACA	ATC	AAC	CGA
gly	ser	gly	ser	gly	thr	ser	tyr	ser	leu	thr	ile	asn	arg
77	78	79	80	81	82	83	84	85	86	87	88	89	90
ATG	GAG	GCT	GAG	GAT	GCT	GCC	ACT	TAT	TAC	TGC	CAG	GAG	TGG
met	glu	ala	glu	asp	ala	ala	thr	tyr	tyr	cys	gln	glu	trp
91	92	93	94	95	96	97	98	99	100	101	102	103	
AGT	GGT	TAT	CCG	TAC	ACG	TTC	GGA	GGG	GGG	ACA	AAG	TTG	
ser	gly	tyr	pro	tyr	thr	phe	gly	gly	gly	thr	lys	leu	

2025-12-20 10:20:00

Fig. 3B

[illegible]

15.03.00



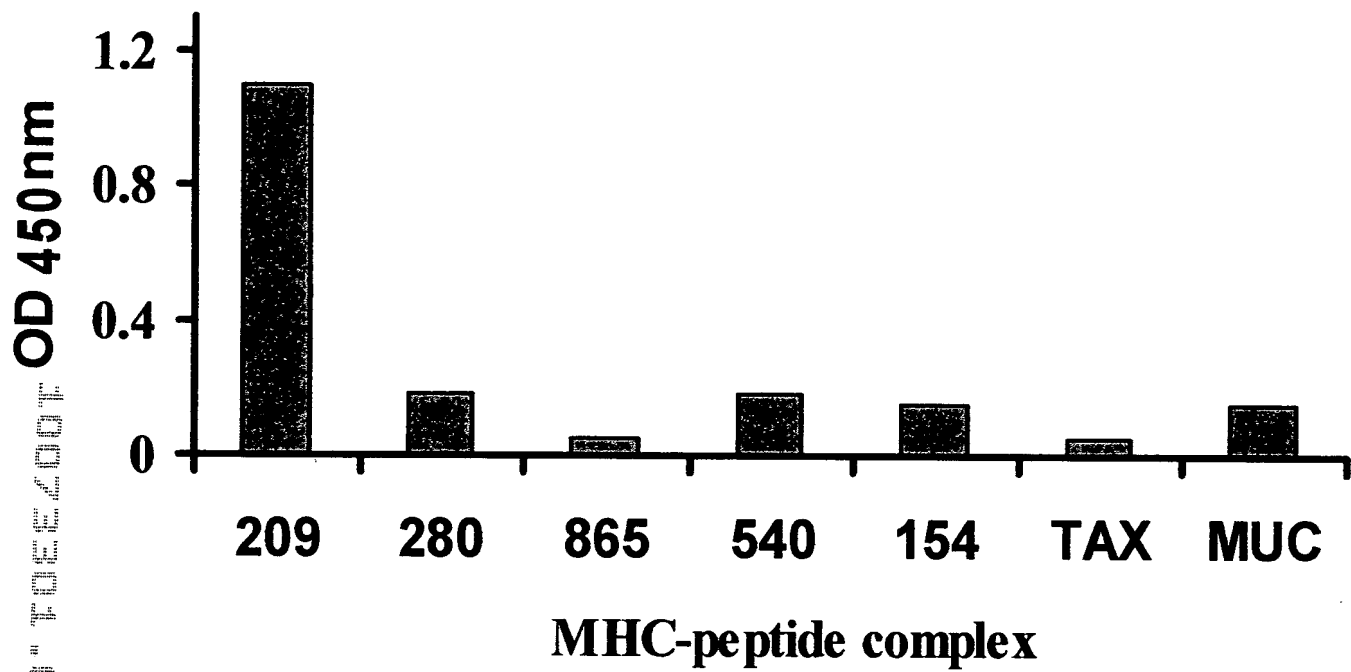


Fig. 4

2007-07-20 10:00:00

Fig. 5A

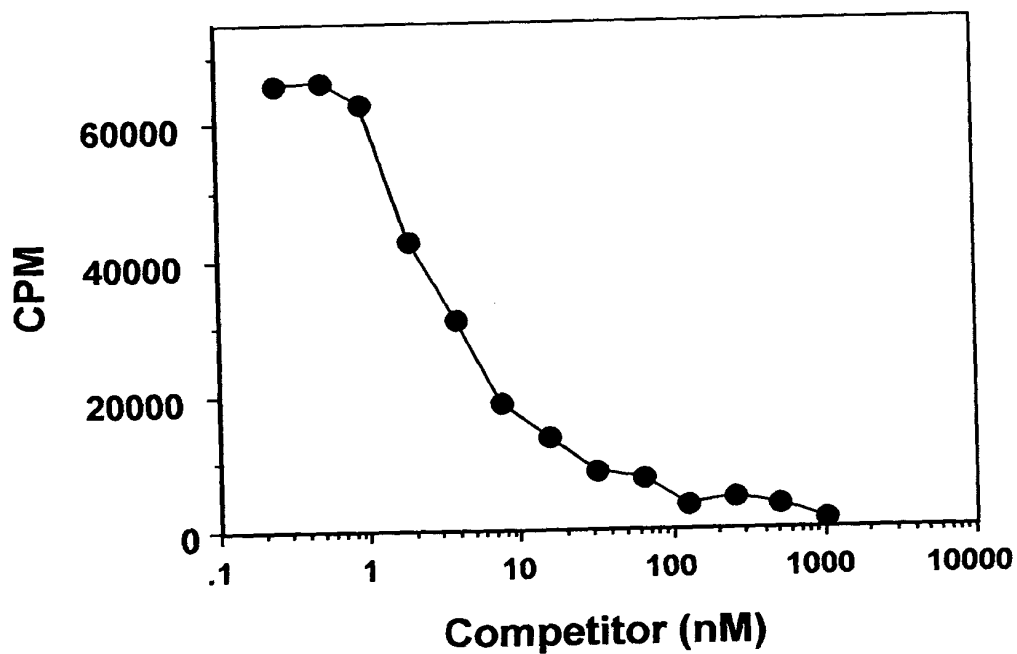
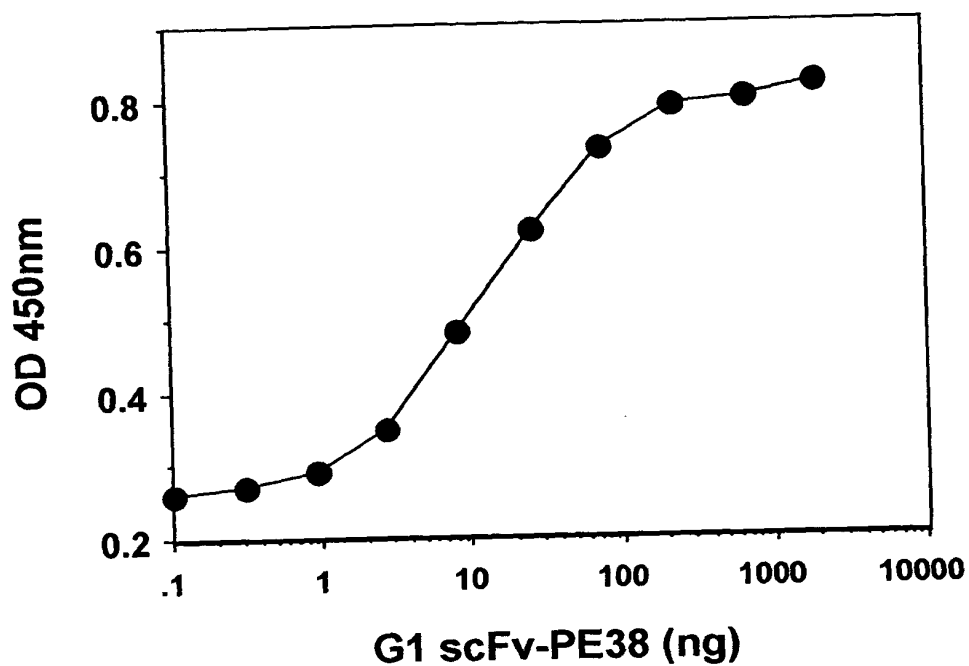
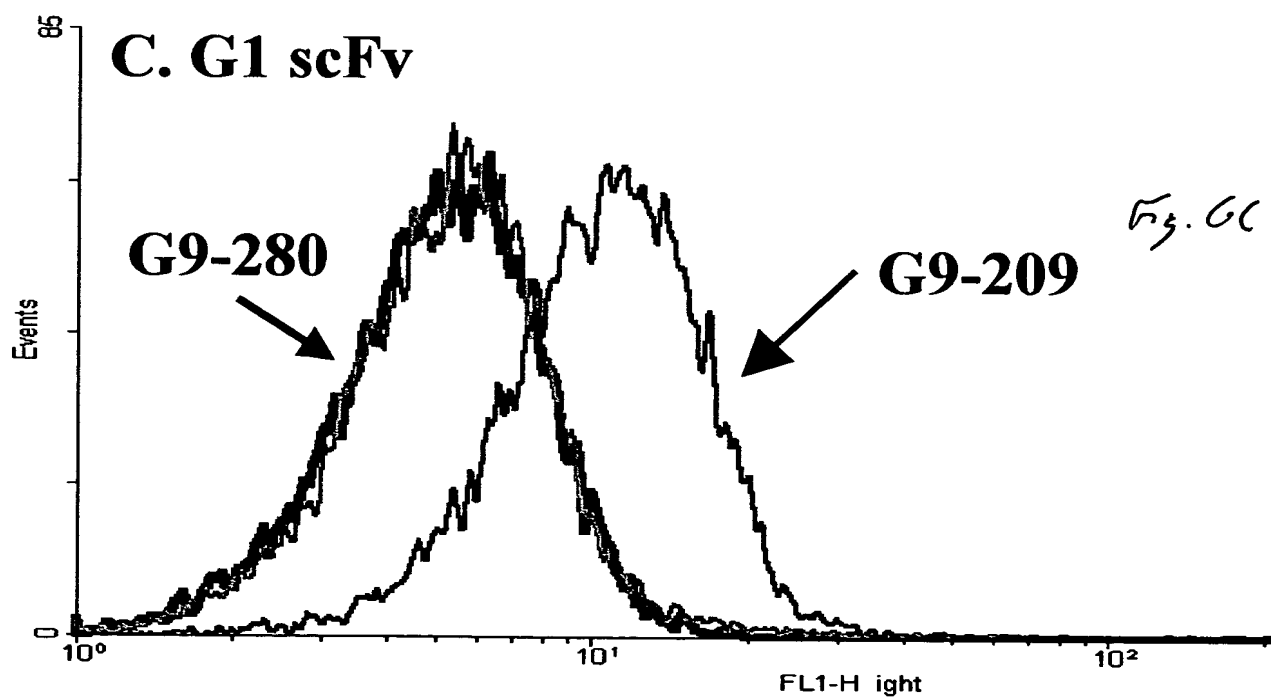
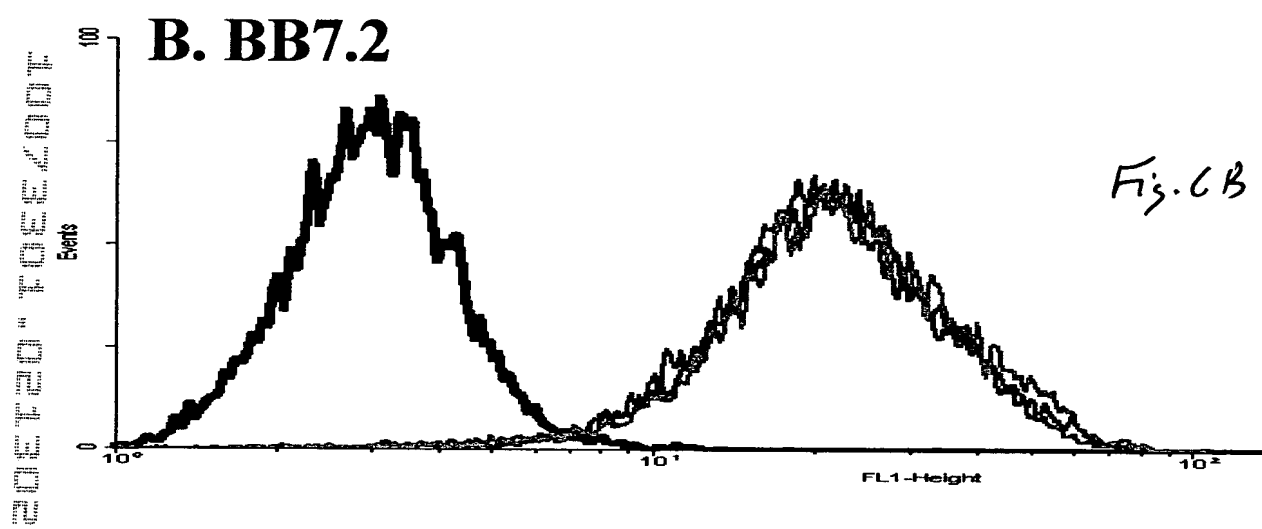
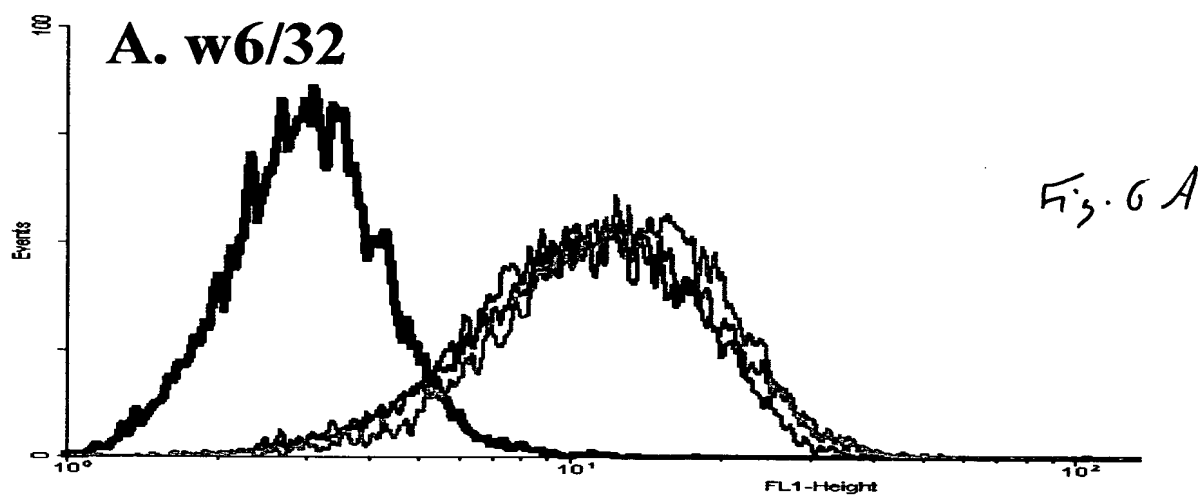


Fig. 5B



Protein synthesis (% of control)

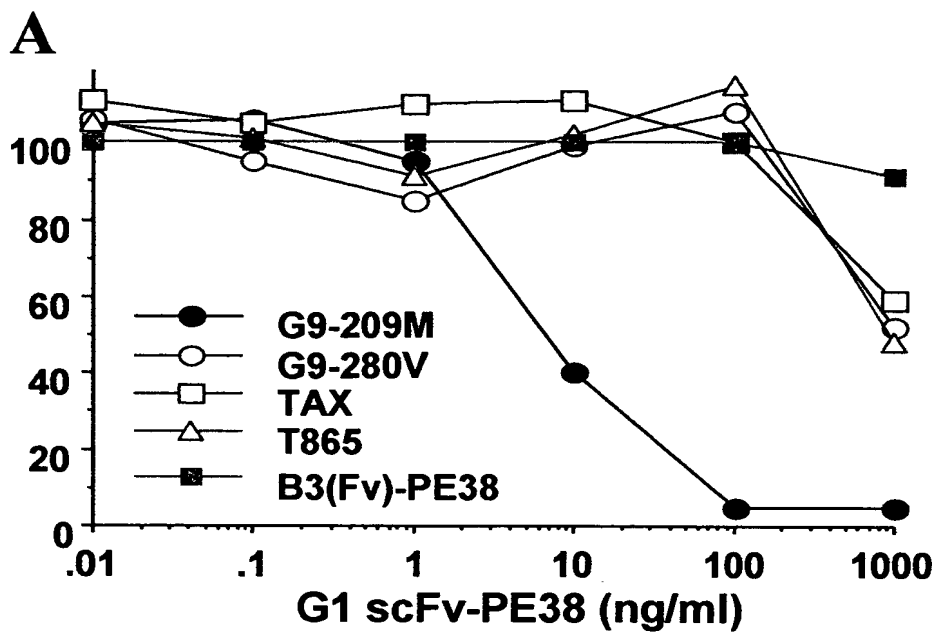


Fig. 7A

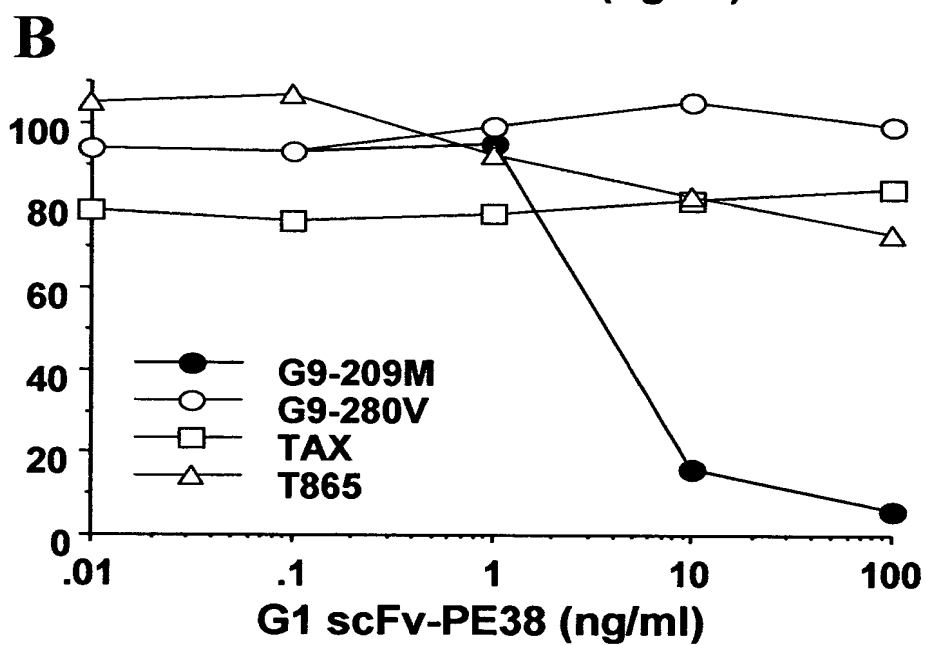


Fig. 7B

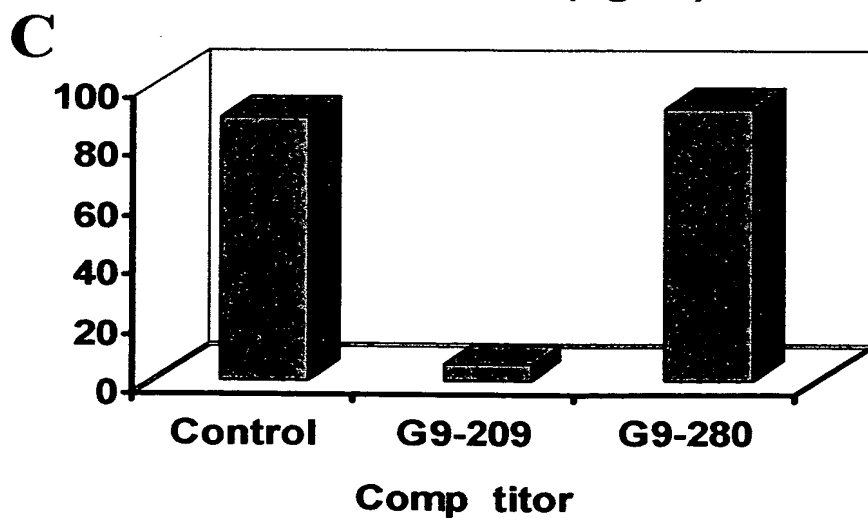


Fig. 7C